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## RAW SEQUENCE LISTING

DATE: 08/25/2004

PATENT APPLICATION: US/10/645,085A

TIME: 15:36:23

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Output Set: N:\CRF4\08252004\J645085A.raw

3 <110> APPLICANT: FUKUSHIMA, NAOSHI  
 4 TSUCHIYA, MASAYUKI  
 5 OH-EDA, MASAYOSHI  
 6 UNO, SHINSUKE  
 7 KIKUCHI, YASUFUMI  
 8 OHTOMO, TOSHIHIKO  
 10 <120> TITLE OF INVENTION: AGONIST ANTIBODIES  
 12 <130> FILE REFERENCE: 065678-0108  
 14 <140> CURRENT APPLICATION NUMBER: 10/645,085A  
 C--> 15 <141> CURRENT FILING DATE: 2002-10-07  
 17 <150> PRIOR APPLICATION NUMBER: PCT/JP01/03288  
 18 <151> PRIOR FILING DATE: 2001-04-17  
 20 <150> PRIOR APPLICATION NUMBER: PCT/JP01/01912  
 21 <151> PRIOR FILING DATE: 2001-03-12  
 23 <150> PRIOR APPLICATION NUMBER: JP 2000-115246  
 24 <151> PRIOR FILING DATE: 2000-04-17  
 26 <150> PRIOR APPLICATION NUMBER: JP 2000-321821  
 27 <151> PRIOR FILING DATE: 2000-10-20  
 29 <150> PRIOR APPLICATION NUMBER: JP 2000-321822  
 30 <151> PRIOR FILING DATE: 2000-10-20  
 32 <160> NUMBER OF SEQ ID NOS: 138  
 34 <170> SOFTWARE: PatentIn Ver. 3.2  
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 39 <213> ORGANISM: Artificial Sequence  
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 42 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
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 62 <212> TYPE: DNA  
 63 <213> ORGANISM: Artificial Sequence  
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87 <213> ORGANISM: Mus musculus
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91 <222> LOCATION: (1)..(393)
92 <223> OTHER INFORMATION: pGEM-M1L. 1-57; signal peptide, 58-394; mature peptide
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96 Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
97 1 5 10 15
99 tcc agc agt gat gtt gtg atg acc caa act cca ctc tcc ctg cct gtc 96
100 Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
101 20 25 30
103 agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt 144
104 Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
105 35 40 45
107 cta cac agt aaa gga aac acc tat tta caa tgg tac cta cag aag cca 192
108 Leu His Ser Lys Gly Asn Thr Tyr Leu Gln Trp Tyr Leu Gln Lys Pro
109 50 55 60
111 ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct 240
112 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
113 65 70 75 80
115 ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca 288
116 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
117 85 90 95
119 ctc aag atc agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc 336
120 Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
121 100 105 110
123 tct caa agt aca cat gtt ccg tac acg tcc gga ggg ggg acc aag ctg 384
124 Ser Gln Ser Thr His Val Pro Tyr Thr Ser Gly Gly Gly Thr Lys Leu
125 115 120 125
127 gaa ata aaa c 394
128 Glu Ile Lys
129 130
132 <210> SEQ ID NO: 6
133 <211> LENGTH: 409

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139 <222> LOCATION: (1)..(408)
140 <223> OTHER INFORMATION: pGEM-M1H. 1-57; signal peptide, 58-408; mature peptide
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145 1 5 10 15
147 gtc cac tcc cag gtc cag ctg cag cag tct gga cct gac ctg gta aag 96
148 Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys
149 20 25 30
151 cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc 144
152 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
153 35 40 45
155 gtt aac cat gtt atg cac tgg gtg aag cag aag cca ggg cag ggc ctt 192
156 Val Asn His Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
157 50 55 60
159 gag tgg att gga tat att tat cct tac aat gat ggt act aag tac aat 240
160 Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
161 65 70 75 80
163 gag aag ttc aag ggc aag gcc aca ctg act tca gag aaa tcc tcc agc 288
164 Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Glu Lys Ser Ser Ser
165 85 90 95
167 gca gcc tac atg gag ctc agc agc ctg gcc tct gag gac tct gcg gtc 336
168 Ala Ala Tyr Met Glu Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val
169 100 105 110
171 tac tac tgt gca aga ggg ggt tac tat agt tac gac gac tgg ggc caa 384
172 Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Ser Tyr Asp Asp Trp Gly Gln
173 115 120 125
175 ggc acc act ctc aca gtc tcc tca g 409
176 Gly Thr Thr Leu Thr Val Ser Ser
177 130 135
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182 <212> TYPE: DNA
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185 <220> FEATURE:
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187 <222> LOCATION: (1)..(393)
188 <223> OTHER INFORMATION: pGEM-M2L. 1-57; signal peptide, 58-393; mature peptide
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192 Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Gly
193 1 5 10 15
195 tcc agc agt gat gtt gtg atg acc caa agt cca ctc tcc ctg cct gtc 96
196 Ser Ser Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val
197 20 25 30

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199 agt ctt gga gat caa gcc tcc atc tct tgc aga tca agt cag agc ctt 144
200 Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
201      35      40      45
203 gtg cac agt aat gga aag acc tat tta cat tgg tac ctg cag aag cca 192
204 Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
205      50      55      60
207 ggc cag tct cca aaa ctc ctg atc tac aaa gtt tcc aac cga ttt tct 240
208 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
209 65      70      75      80
211 ggg gtc cca gac agg ttc agt ggc agt gga tca gtg aca gat ttc aca 288
212 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Val Thr Asp Phe Thr
213      85      90      95
215 ctc atg atc agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc 336
216 Leu Met Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
217      100      105      110
219 tct caa agt aca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg 384
220 Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
221      115      120      125
223 gaa ata aaa c 394
224 Glu Ile Lys
225      130
228 <210> SEQ ID NO: 8
229 <211> LENGTH: 409
230 <212> TYPE: DNA
231 <213> ORGANISM: Mus musculus
233 <220> FEATURE:
234 <221> NAME/KEY: CDS
235 <222> LOCATION: (1)..(408)
236 <223> OTHER INFORMATION: pGEM-M2H. 1-57; signal peptide, 58-408; mature peptide
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240 Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Ser Gly Thr Ala Gly
241 1      5      10      15
243 gtc cac tcc cag gtc cag ctg cag cag tct gga cct gaa ctg gta aag 96
244 Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
245      20      25      30
247 cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc 144
248 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
249      35      40      45
251 gct aac cat gtt att cac tgg gtg aag cag aag cca ggg cag ggc ctt 192
252 Ala Asn His Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
253      50      55      60
255 gag tgg att gga tat att tat cct tac aat gat ggt act aag tat aat 240
256 Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
257 65      70      75      80
259 gag aag ttc aag gac aag gcc act ctg act tca gac aaa tcc tcc acc 288
260 Glu Lys Phe Lys Asp Lys Ala Thr Leu Ser Asp Lys Ser Ser Thr
261      85      90      95
263 aca gcc tac atg gac ctc agc agc ctg gcc tct gag gac tct gcg gtc 336

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## RAW SEQUENCE LISTING

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264 Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val
265          100          105          110
267 tat tac tgt gca aga ggg ggt tac tat act tac gac gac tgg ggc caa 384
268 Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln
269          115          120          125
271 ggc acc act ctc aca gtc tcc tca g 409
272 Gly Thr Thr Leu Thr Val Ser Ser
273          130          135
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284 <400> SEQUENCE: 9
285 cccaagcttc caccatgaag ttgcctgtta gg 32
288 <210> SEQ ID NO: 10
289 <211> LENGTH: 32
290 <212> TYPE: DNA
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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300 <210> SEQ ID NO: 11
301 <211> LENGTH: 34
302 <212> TYPE: DNA
303 <213> ORGANISM: Artificial Sequence
305 <220> FEATURE:
306 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
308 <400> SEQUENCE: 11
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312 <210> SEQ ID NO: 12
313 <211> LENGTH: 34
314 <212> TYPE: DNA
315 <213> ORGANISM: Artificial Sequence
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318 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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325 <211> LENGTH: 30
326 <212> TYPE: DNA
327 <213> ORGANISM: Artificial Sequence
329 <220> FEATURE:
330 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
332 <400> SEQUENCE: 13
333 catgccatgg cgcaggtcca gctgcagcag 30
336 <210> SEQ ID NO: 14

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VERIFICATION SUMMARY

DATE: 08/25/2004

PATENT APPLICATION: US/10/645,085A

TIME: 15:36:25

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